

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 7, 2002, 15:37:26 ; Search time 101.88 Seconds

(without alignments)
462,072 Million cell updates/sec

Title: US-08-569-749-2

Perfect score: 3277

Sequence: 1 MKRTASQRLFPGPSYONIKS.....LRKPCRCIKGIKTVTFPLS 618

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :
1: PIR_68:4
2: PIR1:
3: PIR2:
4: PIR3:
5: PIR4:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3247	99.1	618	2	S68450 apoptos is inhibito
2	2332	71.2	604	2	S68449 apoptos is inhibito
3	1532	46.8	358	2	JC5964 apoptos is inhibito
4	908	27.7	497	2	S69544 apoptos is inhibito
5	737	22.5	497	2	S69545 apoptos is inhibito
6	723.5	22.1	496	2	S68452 apoptos is inhibito
7	513	15.7	268	2	T10304 inhibitor of apopt
8	513	15.7	268	2	A51989 apoptos is inhibito
9	468	14.3	1447	2	T42628 neuronal apoptos is
10	463	14.1	1232	2	A55478 neuronal apoptos is
11	453	14.1	375	2	A54679 inhibitor of apopt
12	400.5	14.1	398	3	JC7568 kidney inhibito
13	237.40	7.2	692	2	T43523 IAP1 or I21 - Bomby
14	237.3	7.2	286	2	D36828 orf13 protein - Au
15	223.5	6.8	275	2	T10310 apoptos is inhibito
16	184	5.7	4845	2	T31067 BIR repeat contain
17	184	5.7	316	2	T32659 hypothetical prote
18	181.5	5.5	711	2	C84767 hypothetical prote
19	175.5	5.2	208	2	T03183 Orf MSY248 probabl
20	169	5.0	150	2	T28409 rmgB protein, cyto
21	165	5.0	943	2	S68824 apoptos is inhibito
22	161	4.9	155	2	T30489 protein F15K9.3 (i
23	156	4.8	823	2	D86165 probable apoptos is
24	152	4.6	234	2	T30427 hypothetical prote
25	152	4.6	304	2	T04751 hypothetical prote
26	146	4.4	870	2	G86450 apoptos is inhibito
27	146	4.4	249	2	H72858 IAP2 orf71 - Bomby
28	144	4.3	249	2	T41814
29	142	4.3	249	2	T41814

30	140.5	4.3	785	2	T00474 hypothetical prote
31	138	4.2	372	2	C96631 hypothetical prote
32	137.5	4.2	236	2	T10343 inhibitor of apopt
33	137	4.2	614	2	S42526 finger protein unk
34	136.5	4.2	854	2	T01393 apoptos is inhibito
35	131.5	4.0	899	2	D96594 unknown protein, 7
36	131	4.0	308	2	T37474 apoptos is inhibito
37	130	4.0	115	2	B96664 probable RING zinc
38	129.5	4.0	329	2	T28403 Orf MSY242 probabl
39	128	3.9	247	2	T01044 hypothetical prote
40	126	3.9	1639	2	T50119 probable sensor, c
41	126	3.8	145	2	S77736 hypothetical zinc fing
42	124.5	3.8	383	2	F96582 hypothetical prote
43	122	3.7	2364	2	T40884 cytochrome L - Clos
44	121.5	3.7	708	2	T00064 hypothetical prote
45	121.5	3.7	739	2	E86434 protein f17f8.27 1

ALIGNMENTS

RESULT 1
S68450 apoptos is inhibitor hlap-2 - human
C:Species: Homo sapiens (man)
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 21-Jul-2000
C:Accession: S68450
C:History: P.: Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Chertton-Horvat, G.; Faraha
Nature 379, 349-353, 1996
A:Title: Suppression of apoptosis in mammalian cells by Nalp and a related family of
A:Reference number: A58182; MUID:96149249
A:Accession: S68450
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-618 <LIS>
A:Cross-References: EMBL:U45879; NID:91184317; PIDN:MAC50372.1; PID:91184318
C:Function:
A:Description: apoptotic suppressor
C:Superfamily: RING finger homology
C:Keywords: apoptos is; zinc finger
F:567-611/Domain: RING finger homology <RNG>

Query Match 99.1%; Score 3247; DB 2; Length 618;
Best Local Similarity 99.4%; Pred. No. 1.3e-216;
Matches 614; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 1 MKRTASQRLFPGPSYONIKSIMESTIISOMTNSNKKMKKYDFSCELYRMSYSTPPAGY 60
|||||
DB 1 MKRTASQRLFPGPSYONIKSIMEDSTILSDMTNSNKKMKKYDFSCELYRMSYSTPPAGY 60
OY 61 PVSRSLARAGFYTGVDNKKVCFCCGLMDNMKLDSPITQKHQLYPSCFTQNLVSN 120
|||||
DB 61 PVSRSLARAGFYTGVDNKKVCFCCGLMDNMKLDSPITQKHQLYPSCFTQNLVSN 120
OY 121 LSTSKTSPKRNFAHSLPTLEHSLFSGSYSLSPNLSRAVEDISSRPNYSYA 180
|||||
DB 121 LSTSKTSPKRNFAHSLPTLEHSLFSGSYSLSPNLSRAVEDISSRPNYSYA 180
OY 181 MSTEARTLYHMPPLTFSSEELARAGFYICPGDRAVCFCCGKLSNMPPKDDMSH 240
|||||
DB 181 MSTEARTLYHMPPLTFSSEELARAGFYICPGDRAVCFCCGKLSNMPPKDDMSH 240
OY 241 RHFPNCPLENSLETIRFSISNLSMOTHAARKRTFMYPSVPQPOLASAGFYVGR 300
|||||
DB 241 RHFPNCPLENSLETIRFSISNLSMOTHAARKRTFMYPSVPQPOLASAGFYVGR 300
OY 301 NDVACFCFCCDGLRCWESDDDPVHEANRPCEFLIRKKGDFVDEIGRYPHLLBOLL 360
|||||
DB 301 NDVACFCFCCDGLRCWESDDDPVHEANRPCEFLIRKKGDFVDEIGRYPHLLBOLL 360
OY 361 STSDTGTGENADPEIIFGFGESSEDAVMMNTPVVSALEKGFNRDLVKQVOSKILTF 420
|||||

Db 361 STSDTTEENADPPIHFGPCESSBDVAVMNTPVYKSALEKMGFNRLVQTVLSKILT 420
Oy 421 GENYKTVNDIYVALLNAEDEKREEKEAEMASDDLILIRKNRMAALFOOLTCVLTLD 480
Db 421 GENYKTVNDIYVALLNAEDEKREEKEAEMASDDLILIRKNRMAALFOOLTCVLTLD 480
Oy 481 NLKANVINIKOHOIIOKOTQIPLQARELIDITLVKGNMAANIFKNCJKEIDSTLYKNLP 540
Db 481 NLKANVINIKOHOIIOKOTQIPLQARELIDITLVKGNMAANIFKNCJKEIDSTLYKNLP 540
Oy 541 VDKNMKYIPTEDVSGLSLEBOLRLQOEPTCYCKMDKESVYVIFPGHLYVQCEAPSLR 600
Db 541 VDKNMKYIPTEDVSGLSLEBOLRLQOEPTCYCKMDKESVYVIFPGHLYVQCEAPSLR 600
Oy 601 KCPICGIIKGTVTFELS 618
Db 601 KCPICGIIKGTVTFELS 618

RESULT 2

568449
Apoptosis inhibitor hlap-1 - human
C:Species: Homo sapiens (man)
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 21-Jul-2000
C:Accession: S68449
R:Liston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Chertton-Horvat, G.; Farhani, Nature 379, 349-353, 1996
A:Title: Suppression of apoptosis in mammalian cells by NAIP and a related family of IAP
A:Reference number: A58182; MUID:96149249
A:Accession: S68449
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-604 <LIS>
A:Cross-references: EMBL:U45878; NID:g1184315; PIDN:AC50371.1; PID:g1184316
C:Function:
A:Description: apoptotic suppressor
C:Superfamily: RING finger homology
C:Keywords: apoptosis; zinc finger
F:551-597/Domain: RING finger homology <RNG>

Query Match 71.2% Score 2332; DB 2; Length 604;
Best local similarity 72.1% Pred. No. 2-2e-153;
Matches 435; Conservative 72; Mismatches 92; Indels 4; Gaps 4;
Oy 20 STMEDSTILSDKTNK -HKQAKYDSCLELYPMSTYSTEPAQVPSERSLARAGFYTVG 78
Db 2 NIVENSIFLSNLSKMSANTFELKTDSCLELYPMSTYSTEPAQVPSERSLARAGFYTVG 61
Oy 79 DAVKCFCCGLMDNMKLGDSPIQIKHQLYPCSCFIQNLVSA -SLGTSKNTSPMRNSFA 136
Db 62 DAVKCFCCGLMDNMKLGDSPIQIKHQLYPCSCFIQNLVSA -SLGTSKNTSPMRNSFA 121
Oy 137 HSLSPTEBHSLSFGSYSSLSPPNLSNRAVEDISSRTNPFYSYAMSTEAREFLTYHMMPL 196
Db 122 HSLSPTEBHSLSFGSYSSLSPPNLSNRAVEDISSRTNPFYSYAMSTEAREFLTYHMMPL 181
Oy 197 TFLSPSELARAGFYIIGPGRVACFACGKLSNNEPKDAMSEHRRHPNCPFLTENSL-E 255
Db 182 TFLSPSELARAGFYIIGPGRVACFACGKLSNNEPKDAMSEHRRHPNCPFLTENSL-D 241
Oy 256 TFLSPSELARAGFYIIGPGRVACFACGKLSNNEPKDAMSEHRRHPNCPFLTENSL-E 315
Db 242 TFLSPSELARAGFYIIGPGRVACFACGKLSNNEPKDAMSEHRRHPNCPFLTENSL-D 301
Oy 316 MESGDDPMVYHAKKFPFCEFLIRKMGOFVDEIGRYPHILDEQLSTSDTTEENADPPI 375
Db 302 MESGDDPMVYHAKKFPFCEFLIRKMGOFVDEIGRYPHILDEQLSTSDTTEENADPPI 361
Oy 376 IHFGGSESSRDAYNMNTPVYKSALEKMGFNRLVQTVLSKILTGENYKTVNDIYVALL 435
Db 362 IHFGGSESSRDAYNMNTPVYKSALEKMGFNRLVQTVLSKILTGENYKTVNDIYVALL 421

Oy 436 NARDEKREEKEAEMASDDLILIRKNRMAALFOOLTCVLTLDNLKANVINIKOHOI 495
Db 422 NARDEKREEKEAEMASDDLILIRKNRMAALFOOLTCVLTLDNLKANVINIKOHOI 481
Oy 496 IKOKOTQIPLQARELIDITLVKGNMAANIFKNCJKEIDSTLYKNLPVYKMKYIPTEDVSG 555
Db 482 IKOKOTQIPLQARELIDITLVKGNMAANIFKNCJKEIDSTLYKNLPVYKMKYIPTEDVSG 541
Oy 556 LSLBOLRLQOEPTCYCKMDKESVYVIFPGHLYVQCEAPSLRKPICGIIKGTVTF 615
Db 542 LSLBOLRLQOEPTCYCKMDKESVYVIFPGHLYVQCEAPSLRKPICGIIKGTVTF 601
Oy 616 FLS 618
Db 602 FLS 604

RESULT 3

JC5964
Apoptosis inhibitor - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 02-Sep-2000
C:Accession: JC5964
R:Stechlik, C.; de Martin, R.; Binder, B.R.; Lippe, J. Biochem. Biophys. Res. Commun. 243, 827-832, 1998
A:Title: Cytokine induced expression of porcine inhibitor of apoptosis protein (Iap)
A:Reference number: JC5964; MUID:98162822
A:Accession: JC5964
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-358 <STFE>
A:Cross-references: GB:U79142; NID:92957174; PIDN:AC39171.1; PID:92957175
C:Superfamily: RING finger homology
F:307-351/Domain: RING finger homology <RRN>

Query Match 46.8% Score 1532; DB 2; Length 358;
Best local similarity 65.1% Pred. No. 2e-98; 33; Indels 82; Gaps 2;
Matches 286; Conservative 98; Mismatches 33; Indels 82; Gaps 2;
Oy 181 MSTEAREFLTYHMMPLTFLSPSELARAGFYIIGPGRVACFACGKLSNNEPKDAMSEH 240
Db 1 MSTEAREFLTYHMMPLTFLSPSELARAGFYIIGPGRVACFACGKLSNNEPKDAMSEH 60
Oy 241 RRRHPNCPFLTENSL-ETLRPSISNLSMOTHAARMTFWPSSVYVQPEOLASAGFYTVG 299
Db 61 RRRHPNCPFLTENSL-ETLRPSISNLSMOTHAARMTFWPSSVYVQPEOLASAGFYTVG 120
Oy 300 RNDVYKCECCOGSLRWESGDDPMVYHAKKFPFCEFLIRKMGOFVDEIGRYPHILDEQL 359
Db 121 RNDVYKCECCOGSLRWESGDDPMVYHAKKFPFCEFLIRKMGOFVDEIGRYPHILDEQL 180
Oy 360 LSTSDTTEENADPPIHFGPCESSBDVAVMNTPVYKSALEKMGFNRLVQTVOSKILT 419
Db 181 LSTSDTTEENADPPIHFGPCESSBDVAVMNTPVYKSALEKMGFNRLVQTVOSKILT 195
Oy 420 TGENYKTVNDIYVALLNAEDEKREEKEAEMASDDLILIRKNRMAALFOOLTCVLT 479
Db 196 TGENYKTVNDIYVALLNAEDEKREEKEAEMASDDLILIRKNRMAALFOOLTCVLT 219
Oy 480 NLKANVINIKOHOIIOKOTQIPLQARELIDITLVKGNMAANIFKNCJKEIDSTLYKNLP 539
Db 220 NLKANVINIKOHOIIOKOTQIPLQARELIDITLVKGNMAANIFKNCJKEIDSTLYKNLP 279
Oy 540 FVDKMKYIPTEDVSGLSLEBOLRLQOEPTCYCKMDKESVYVIFPGHLYVQCEAPSLR 599
Db 280 FVDKMKYIPTEDVSGLSLEBOLRLQOEPTCYCKMDKESVYVIFPGHLYVQCEAPSLR 539
Oy 600 KCPICGIIKGTVTFELS 618
Db 340 KCPICGIIKGTVTFELS 358

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RESULT 4
569544
apoptosis inhibitor IAP homolog - human
C:Species: Homo sapiens (man)
C>Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 17-Nov-2000
C:Accession: S69544; S68451
R:Duckett, C.S.; Nava, V.E.; Gedrich, R.W.; Clem, R.J.; van Dongen, J.L.; Giffillan, M.C
EMBO J. 15, 2685-2694, 1996
A:Title: A conserved family of cellular genes related to the baculovirus iap gene and er
A:Reference number: S69544; MUID:96256286
A:Accession: S69544
A>Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-497 <DDC>
A:Cross-references: EMBL:U32974; NID:91016687; PIDN:AC050518.1; PID:91016688
R:Liston, P.; Roy, N.; Tamai, K.; Letebvre, C.; Baird, S.; Chertton-Horvat, G.; Farhani,
Nature 379, 349-353, 1996
A:Title: Suppression of apoptosis in mammalian cells by NAIP and a related family of IAP
A:Reference number: A50182; MUID:96149249
A:Accession: S68451
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-161 'C', 163-422, 'O', 424-497 <LIS>
A:Cross-references: EMBL:U45880; NID:91104319; PIDN:AC050373.1; PID:91104320
C:Genes: 11P
A:Gene: 11P
C:Function: 11P
A:Description: 11P: apoptotic suppressor
C:Superfamily: 11P: apoptosis inhibitor IAP homolog: RING finger homology
C:Keywords: 11P: apoptosis; zinc finger
F:446-490/Domain: RING finger homology <RRN>

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Query Match 27.7%: Score 908; DB 2; Length 497;
Best Local Similarity 33.8%; Pred. No. 4,4e-53;
Matches 205; Conservative 88; Mismatches 164; Indels 150; Gaps 14;

QY 35 MKKKMIDPSCGLYRMSTYTPAGVPYSEKSLARAGTYTGNDKVKCFCCGLMDNKK 94
DB 18 MKEE--EVEEFNRLKTFANFPSSPVASSTLARAQVLTGDPVCFSCIAAADRMQ 74
QY 95 LGDSPLOKHQQLPSCSFIONLVASLSGSTSKNTSPMRNSF-AHSLSPTLEHSLPESGY 153
DB 75 YGDSAVGRHRYVSPNCRFINGFYLENSATOSTNSGIONGVKENVLGSRDHFLDRPS- 133
QY 154 SSLSPNPLNSRAVEDISSHTNPYSYAMSTEAFRLTYHWP-LTFLSPSLARAGTYT 212
DB 134 ETDADYLTGQVVDISDT-IYRNPAMYSEBARLKSFQWMPDYAHATPRELASAGLYYT 192
QY 213 GPGDRVACFACGKLSMWBKDDANSEHRHFPNCPPL- - - - -EN 252
DB 193 GIDQVOCFCGCGKIKMWBKDDANSEHRHFPNCPFLVGLRLNLTIRSSDAVSSDRNFPN 252
QY 253 SLETLRFSTLSMOTHAAMRTFMYWPSYVQPEOLASAGFYVGRNDVKCFCCDGG 312
DB 253 STYLPR---NPSMADYEARIFFPGTWIYS--VNBKDLANAGYVALGEGEDVKCFHCGG 306
QY 313 LRCMGGDPWVEHAKWFPCEFLIRMGQEFVDEIGRYPHLLD-LLSTSDTTGEEM 371
DB 307 LTMKRSBDMPOHAKWFPCKCYLLEOKOEYINNI--HLTHGLCELVARTTEKT----- 359
QY 372 DPEIHFPGSESSDAVMMNTPYVKSALENGPNRDVYKQYOSKILTTGENTYVDYI 431
DB 360 -----PSLTRRIDDTIFQNPVDEALRMGFSKDKIKIMBEKIOISGYSKLEVL 411
QY 432 SALLNMEDEKREEREKEQAEASDLSLRKRNMAFLQOLTCVPLTLDNLKANVINKO 491
DB 412 ADLVNKKDSMPDE----- 425
QY 492 EHDITKQTOPIQARELIDTILVKGNAANIFKMKLEIDSTLYKNLFPVOKNMKYIPE 551
DB 426 -----SSQSTSLQ-----KEI----- 435

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QY 552 DVSGLSLEEDLRRLQERTCKVCKMOKESVVFIPCGHLVVCQCAPSLKRCPIGCIKG 611
DB 436 -----STEEORLRLQEGEKLCKICMDRNIAIVFPCGHLVTCQCAEAVNDKPCWCVITTF 490
QY 612 TVRFPS 618
DB 491 KQIKIMS 497

RESULT 5
569545
apoptosis inhibitor IAP homolog - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C>Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C:Accession: S69545
R:Duckett, C.S.; Nava, V.E.; Gedrich, R.W.; Clem, R.J.; van Dongen, J.L.; Giffillan,
EMBO J. 15, 2685-2694, 1996
A:Title: A conserved family of cellular genes related to the baculovirus iap gene and
A:Reference number: S69544; MUID:96256286
A:Accession: S69545
A>Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-497 <DDC>
A:Cross-references: EMBL:U32373; NID:91019116; PIDN:AC047155.1; PID:91019117
C:Genes: 11P
A:Gene: 11P
C:Superfamily: 11P: apoptosis inhibitor IAP homolog: RING finger homology
F:446-490/Domain: RING finger homology <RRN>

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Query Match 22.5%: Score 737; DB 2; Length 497;
Best Local Similarity 30.6%; Pred. No. 2.9e-43;
Matches 180; Conservative 82; Mismatches 212; Indels 114; Gaps 15;

QY 46 ELYRSTYTPAGVYSEKSLARAGTYTGNDKVKCFCCGLMDNKKLGDSPLQKHO 105
DB 9 ESYRLATGEMPLANRYSAEDLVANGFATQNMLEACFPCHVRIDREHGGDVAAGHR 68
QY 106 LTPSCFIONLVASLSGSTSKNTSPMRNSFPHLSLPTLEHSLPESGYSSLSPNLSRA 165
DB 69 SPTLSMV--LAPNHCNVPR-----SOESDNEGS-- 97
QY 166 VEDISSHTNPYSYAMSTEAFRLTYHWP-LTFLSPSLARAGTYTIGPDRAVACAGG 225
DB 98 VVDSFSCSP--DLLEANNRLVTFKDPMPNITFQALAKAGTYTLNRKLDIKYCWNG 154
QY 226 KLSMNPDPDAMSEHRHFPNCPPL- - - - -NSLETLRFSTLSMOTH--AA 271
DB 155 VLAKEKMDNAFEBHKEFPQCRVOMGPLEPATGKNLDELGLOPTLPLPKRYACVDA 214
QY 272 RMFTFWPSSVYVQ-EGLASAGFYVGRNDVKCFCCDGLRCMESGDDPWVEHAKW 330
DB 215 RLRTFDWPIIS-NIOPASALDAQGLYVOKIGDOVRCHNIGIKSMOKEDPWEHAKMS 273
QY 331 PCEFLIRMGQEFVDEIGRYPHLLD-LLSTSDTTGEEMAPPIIHPGSESSDAV 390
DB 274 PKQFVPLAKGPSYSEVLA-----TJANASSPPT--APAPTLQADVLM 317
QY 391 MNTPYVKSALENGPNRDVYKQYOSKILTTGENTKYNOTVSALNABDEKREEREKOA 450
DB 318 DEAP-AKELALGIDGGVYRNALQRLSSGCAFSPTDELHLDID----- 362
QY 451 EEMASDLSLRKRNMAFLQOLTCVPLTLDNLKANVINKOEHDIKQTOPIQARELI 510
DB 363 DACACADPMCRASBPAPF-----IEPCOATYSKA-----ASVPVPAVD 403
QY 511 DTLVKGNAANIFKMKLEIDSTLYKNLFPVOKNMKYIPTEDVSGLSLEEDLRLEERT 570
DB 404 PARPQAEAVANISK-----YDEIQRKSVATPAGNLSLEENROLKADRL 449
QY 571 CKVCKMDEKSVVFIPCGHLVVCQCAPSLKRCPIGCIKGTYRTFLS 618
DB 450 CKVCLDEEVGVFLPCGHLATCQCAPSVANCPMRADIKGFVETFLS 497

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RESULT 6

568452
Apoptosis Inhibitor diad - fruit fly (*Drosophila melanogaster*)
C:Species: *Drosophila melanogaster*
C:Date: 17-Jul-1998 #sequence_revision 17-Jun-1998 #text_change 17-Nov-2000
C:Accession: 568452
R:Liston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Chetron-Horvat, G.; Farahani,
Nature 379, 349-353, 1996
A:title: Suppression of apoptosis in mammalian cells by NMP and a related family of INH
A:Reference number: A56187; MIMD:95149249
A:Accession: 568452
A:status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-496 <LIS>
R:Baird, S.D.
A:Cross-References: EMBL:U45881; MIMD:g1184313; PIDD:MAC64586.1; PIDD:g1184314
submitted to the EMBL Data Library, January 1996
A:Reference number: 578528
A:Accession: 578528
A:Molecule type: mRNA
A:Residues: 1-36, AT, 37, 'K', 39, 'L', 41-44, 'K', 46-58, 'Q', 60-412, 'A', 414-427, 'A', 429-496 <
A:Cross-References: EMBL:045881; MIMD:g1184313; PIDD:MAC64586.1; PIDD:g1184314
A:Genetics:
A:Cross-References: FlyBase:FBgn0015247
A:Function:
A:Description: apoptotic suppressor
A:Superfamily: Apoptosis Inhibitor IAP homolog; RING finger homology
A:Keywords: apoptosis; zinc finger
A:445-489/Domain: RING finger homology <RNG>

Query Match	22.1%	Score 723.5	DB 2	Length 496
Best Local Similarity	30.5%	Pred. No. 2.5e-42		
Matches 180	Conservative 90	Mismatches 201	Indels 119	Gaps 18
QY	46	ELYNASTYITFFPGACVPSERSIARACGYTYTGYNQKVCPCCGGLMDLNKLCDSITKHAKO	105	
DB	9	ESVRLIATFGCMLPLNPSVASIEDLVANPFGFTWM--EACDCCHVRIIDREYEDDLVARRHR	66	
QY	106	LVPSCSFTIOWLVASISLIGSTSKNTSPMRNFAHSLSPTLEHSSLFSGSSLSLSPNPENSA	165	
DB	67	SSPITCSWV--LAPNHGQVNPV-----SQSDMEGNS--	95	
QY	166	VEDIISSTNPYSYAMSTEARFLTYHMPLTFISPELARACGYITGPDVYACFACG	225	
DB	96	VYDSDPESCSCP--DLLLEANRLVETKMDPNPNITPOLAKAGFYVILDRHAKCWCWG	121	
QY	226	KLSMWEKDDAMSEARRHFPNCPLE-----NSLETAFSLISLSQTH---AA	271	
DB	153	YJAKNEKMDAEEHRRFPFGCRKNGSLIEFATKCGDCLDELQITPLIRKRYACVYA	212	
QY	272	RHRFTWPPSSVYHNP--EQLSAGAFYGVARNDDYKCCCGGIGRCMGESGDPMWEHAKRF	330	
DB	213	RLRFTDWPIS--NIQASALAGQVIGKQISGVNCHNIGLRMGKEDDPMEHAKMS	271	
QY	331	PPCEFLIRMKGCEVDEIDGRYPHILLEOLLSTISQTEENADPPIIRHGPESSSDAVN	390	
DB	272	PCQCFVLLAGCPAYSEV-----LAL--TAANASSQPAF--APAPITLQDVIM	315	
QY	391	NMTPEVSALEKMFNRDLVKOTVOSKILTTGENTKYNDVSLNLAEDEREKEEXKA	450	
DB	316	DEAP--AKEDALTITIGQGVARNADIRKLSSGCAFSTDELLIHIFPDGAGAAALVERBP	374	
QY	451	EEKMSDDLSTIRKRNMAFLFOOLTGVPIIIDLNLKANIYNIOBHDIKQITQIPL--QARE	508	
DB	375	EPSSA---PPIECQQAITTSKAASVPIPVADS-----IPAKQAAE	410	
QY	509	LIDTILVKGNAANIIFKNCIAEIDSTLYNNLFPVQNMKNIPTREDSVGLSEEQURLQDE	568	
DB	411	-----ANSNISK-----TTDETQKMSVSTPNQNSITLSEENRQLKJA	446	

QY	566	RICKYCKMDEKSVYVEIFPCGHILVWCCDLSLRKQIFIGIRITIGTITRFLS	618
	1	:::	1
Db	447	RICKYCKLDEEVGVFLPCGHILATNCNCCAPSVANCPMCRAIDIGFVTRFLS	496
RESULT	7		
	110304	Inhibitor of apoptosis protein 3 - <i>Orygia pseudotsugata</i> nuclear polyhedrosis virus	
C:Species:	<i>Orygia pseudotsugata</i> nuclear polyhedrosis virus, <i>Opnnpv</i>		
C:Date:	16-Jul-1999	#sequence_revision 16-Jul-1999	#text_change 15-Sep-2000
C:Accession:	U10304		
R:Authors:	G.A.; Russell, R.R.; Funk, C.J.; Evans, J.; Harwood, S.; Rohrmann, G.E.		
V:Title:	The sequence of the <i>Orygia pseudotsugata</i> multinnucleocapsid nuclear polyhedro		
A:Reference number:	Z17011; M01D:97271300		
A:Accession:	U10304		
A:Status:	preliminary; translated from GN/EMBL/DBD/J		
A:Molecule type:	DNA		
A:Residues:	1-268 <NR>		
A:Cross-references:	EMBL:U75930; NID:92934903; PTDN:ACCS9034.1; PTD:91311281		
A:Superfamily:	Viral apoptosis inhibitor JAR; NIM finger homology		
A:[217-261/Domain:	NIM finger homology <NR>		

Query Match	Similarity	15.78	Score 513	DB 2	Length 268
Best Local Similarity	3.24.18	Pred. No. 3.5e-28			
Matches 107	Conservative 51	Mismatches 86	Indels 200	Gaps 4	

Query	181	MSTEEARFELTYHIMPLTFELISPEELARAGFYITGDSHVACFACGGKLSNNMPKDOAMSGH	240
Db	15	MKNKAALIGTYTWMFVQFLEPSNNMAASGFYITLGDSDEVRCACCKVEITNNVNRDDPEIDH	74
Qy	241	RHNEPQPELENSLE-----TLRFSSLSNLSQTLAAAMKMFPMVPSVVPQPEQSLAS	292
Db	75	KMAAOCPEFVRNNADHTPDHARAPARSAAHNHOVATAAALTFPEMRLKQPEELAE	134
Qy	293	AGEEYGRANDYKCFCCDGLRCMESGDDPWEYELAKKFFRCFELLIRMGGEFVDEIQRY	352
Db	135	AAEFETQDGGKRCRCDCDGLKMEBEDDAPMOOAHARYDCFEVLYLKGDFEOR----	189
Qy	353	PHLEQLLSTSDTGTBENADPILHFCQESSSDAVMNFVFSKALEKGFNRDIYKQT	412
Db	190	-----VMEKACVVR-----	198
Qy	413	VDSKLTITGGENTKYNDIVSALLNAEDKREBEKEXKAEEMASDLSLIRKNMALLPOOL	472
Db	199	-----DQNGEHIEBRAYAE-----	214
Qy	473	TCVPLEILDNLKANYINKQEHDIIRKQRIPLQARLELDIILYKNNAAAHIFNCLKEID	532
Db	215	-----	214
Qy	533	SYLTKNLPVDMKNKKIPTEDYSGLSLEBQLRLQLEERTCYCMQDEKVEYVFTGCHLYVC	592
Db	215	-----VADRIACKICLGAEKTYCFVFCRGHYVAC	242
Qy	593	OCBAPSLRKCPICIORIGITKGYATF	616
Db	243	GKCAAGVYTCPCVRCQLODKAVRMV	266

RESULT	8
A53989	
apoptosis-inhibiting protein - Orgyia pseudotsugata multicapsid nuclear polyhedrosis	
C:Species: Orgyia pseudotsugata multicapsid nuclear polyhedrosis virus, OPMNV	
C:Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 15-Sep-2000	
C:Accession: A53989	
R:Birthum, M.J.; Clem, R.J.; Miller, L.K.	
J: J. Virol. 68, 2521-2528, 1994	
A:Title: An apoptosis-inhibiting gene from a nuclear polyhedrosis virus encoding a po	
A:Reference number: A53989; MUID:94187094	
A:Accession: A53989	
A:Status: preliminary	

A: Molecule type: DNA
A: Residues: 1-268 <RRR>
A: Cross-references: GR: L22564; NID: q456111; PIDN: AA802610.1; PID: q456114
A: Note: authors translated the codon TGS for residue 28 as "YR", GAC for residue 50 as As
C: Superfamily: Vflral apoptosis inhibitor IAP; RING finger homology
F: 217-261/Domain: RING finger homology <RRN>

Query Match	15.7%;	Score 513;	DB 2;	Length 268;
Best Local Similarity	24.1%;	Pred. No. 3.5e-28;		
Matches 107;	Conservative 51;	Mismatches 86;	Indels 200;	Gaps 4;

```

OY 181 MSYBARPLVYHMMPLTFUSPEELAPAGVYIGDPRVACFACGKLSNMWERKDAASEH 240
Db 15 MNKMAARLGQTYNNPQPLEPESPMMAAGFYLLRGQGEVACFAFCVELTMMVWGDDPETDH 74
OY 241 RHHPENCFLENSLS-----TLRESISNLSMOTNHAARATRMVPSVSVPCEPOTLS 292
Db 75 KRNAPQCFPVNNNAHNDTPHDAPARSRSAAHNPQYATLEAARLRPPAEPRGLTKORFEELAE 134
OY 293 AGRYVYSGNDPVKPCDCDGLCMSCGDDPMVNAHMPPLREFILRMKCOEFVDEIOGY 352
Db 135 AGPFYTGOGDTRCFCCDGLKDMWEPDDAPMQNARWMDRCEYLLVKGNDPVOR----- 169
OY 353 PHLEQLLSTSDTGEENMDPPIIHFGSGSSSEDAVANNPVYKSALEMGFNBDLVKOT 412
Db 190 -----VMTKACVVR----- 198
OY 413 YQSKILTGTGMYKTVNDIVSALNADERKREBEKEKEMASDLSLRKNRMALPQQL 472
Db 199 -----DADNPIETERRAVANE----- 214
OY 473 TCYLPIDNLNKKANVINKEOHILKQTKQPIAPARLELIDTLVGNMAANIRKNLKEID 532
Db 215 ----- 214
OY 533 STIKKNLEVDNMKNKIYLPEDVAGSLSEQLRLQOEERCKYCMKKEYSVYETPCGHLIYC 592
Db 215 -----VADRLCKTCLDAENYVCFVPCGHVAC 242
OY 593 QECASPLKCPICLIGIITKQTYTF 616
Db 243 GKCAAVTTCVPCNGQIDNAVRYMT 266

```

RESULT 9
T42628
neuronal apoptosis inhibitory protein 2 - mouse
C.Species: Mus musculus (house mouse)
C.Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-Jan-2000
C.Accession: T42628
R.Yarnaghi, Z.; Diez, E.; Gros, P.; Mackenzie, A.
Mamm. Genome 10, 761-763, 1999
A.Title: CDNA cloning and the 5'genomic organization of Nalp2, a candidate gene for mur
A.Reference number: Z22179; MUID:99315342
A.Accession: T42628
A.Status: preliminary; translated from GH/EMBL/DDBJ
A.Molecule type: mRNA
A.Residues: 1-144? <IAB>
A.Cross-references: EMBL:AF102871; NID:93860228; PID:93860229; PTDN:AACT3A002.1
C.GeneInfo:
A:Gene: Nalp2

Query Match Score 468; DB 2; Length 1447;
Best Local Similarity 25.9%; Pred. No. 5,4e-24;
Matches 147; Conservative 73; Mismatches 213; Indels 134; Gaps 19.

01 IMDSPTLL-----SMTAKSNQKQKDFE--CELYRSTYSPFAPGYSVR 65
| : ||||| : : ||||| : | 1 : 1 : 1 :
02 VSLTSLITVALSVLKROOEEDIKRTPKMKGGFGFSOMREAFARKTEFYDEFERSMWFO 79
| : ||||| : : ||||| : | 1 : 1 : 1 :
03 SLARGFFRYGVDMVKCCPCSGAILMDWMKKGASPIQHNNKLDPSCSFDTQLIVASAGISYTS 125

[illegible]

RESULT 10
A:55478
neuronal apoptosis inhibitory protein - human
N:Alternate names: NAIP
C:Species: Homo sapiens (man)
C:Date: 05-Jan-1996 #sequence, revision 05-Jan-1996 #text-change 02-Feb-2001
C:Accession: A55478
R:Roy, N.; Mahdavian, M.S.; McLean, M.; Shuler, G.; Yarnghil, Z.; Farahani, R.; Balut
d, T.O.; de Jong, P.J.; Surh, L.; Ikeda, J.E.; Korneluk, R.G.; Mackenzie, A.
Cell 80, 167-178, 1995
A:Title: The gene for neuronal apoptosis inhibitory protein is partially deleted in 1
A:Reference number: A55478; MIM:95112344
A:Accession: A55478
A:Molecule type: mRNA
A:Residues: 1-1232 <R0Y>
A:Cross-references: GR:U19251
C:Genetics:
A:Gene: GDB:SMA9; SMA
A:Cross-references: GDB:120378; OMIM:600354; OMIM:253300
A:Map positions: Bg12.2-Sq13
C:Keywords: apoptosis; AIP; glycoprotein; nucleotide binding; P-loop; transmembrane P
E:94-110/Domain: transmembrane #status predicted <RMI>
E:470-477/Region: nucleotide-binding motif A (P-loop)
E:478-496/Domain: transmembrane #status predicted <RMI>
E:478/Binding site: AIP (Ays) #status predicted
E:618,632,823,925,1035/Binding site: carboxydrice (asn) (covalent) #status predicted

```

07 Query Match: 14.1%; Score 463; DB 2; Length 1372;
Best Local Similarity: 25.4%; Pred. No. 9; Se 24;
Matches 156; Conservative 90; Identities 146; Gaps 23
07 28 LSPDMSNKSKVADPSCC-----LYMGRVSYFPAGVQSESLKRAQGYFTYVDNK 80
      | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 38 LEEEDQKRRRAQMDKGYNSQMSSEAKRLKTFVYRPEYSWIP--DEMAAGFFFTVWSG 94
      | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
07 81 VQFCGGLMDNNKLDADSTFQKRLQVPCSTQIMVSVASLGSSTKSTSPNNRFAHLS 140

```

[illegible][illegible]

OY 541 VDKNMYIPTEDVSGLSLEBQLRLQEBRTCKVCNDEKVSVPFPCGHLVWCOBCAPSLR 600
 Db 227 -----AMWLEPPGARDVEAQLRLQEBRTCKVCIDRAVSIVPFGCHL-VCACBAPGLQ 280
 OY 601 KCPICGKIGKTVRTFLS 618
 Db 281 LCPICRAVPVRSKRTFLS 298

RESULT 13

1A1P1orf27 - Bombyx mori nuclear polyhedrosis virus (isolate T3)

C:Species: Bombyx mori nuclear polyhedrosis virus, BmNPV

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 15-Sep-2000

C:Accession: T41772

R:Genl: S.; Majima, K.; Maeda, S.

J:Gen. Virol. 80, 1323-1337, 1999

A:Title: Sequence analysis of the genome of Bombyx mori nucleopolyhedrovirus.

A:Reference number: 222020; MUID:99281911

A:Accession: T41772

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-292 <KAM>

A:Cross-references: EMBL:L33180; NID:g3745835; PIDN:AAC63701.1; PID:g3745854

A:Experimental source: isolate T3

C:Genetics:

A:Note: 1A1P1

C:Superfamily: viral apoptosis inhibitor IAP; RING finger homology

Query Match 7.3%; Score 240; DB 2; Length 282;
 Best Local Similarity 18.0%; Pred. No. 3e-09;
 Matches 78; Conservative 41; Mismatches 96; Indels 218; Gaps 9;

OY 208 GFTYIGPGDRVACFACGKLSNNEPKDAMSEHRHFPNCFLENSLETFLRS----- 260
 Db 54 GFYNOVDHVVCEYCEAEIKNMSDECEIYVAHTLSFYCAVANKIAEHSFGDNITINA 113
 OY 261 -----ISNLSMOTHAARMKTFM-VNPSVVPVPEOLASAGFYVYGRNDVK 305
 Db 114 VLVEGRPKCYRCVKNLNQ-----SRMDFFVNMFPALINDITNIAAGLFTGCGDETV 168
 OY 306 CFFCDGGLRCWESGDPMVEHAKMPRCFELIRMGQFVVEIOGRPHILBQLLSTSDT 365
 Db 169 CFFCDGGLRCWESGDPMVEHAKMPRCFELIRMGQFVVEIOGRPHILBQLLSTSDT 209
 OY 366 TGEENMPRIIHFGSESSSDAVMMPTVYKSALEKGFNDLVKQTVOSKILLTGENTK 425
 Db 210 ----- 209
 OY 426 TVMDIVSALLNADEKREKQAEEMASDLSLIRKNRMALFOOLLTCVPLDNLKA 485
 Db 210 -----NAITATTHVDRKDD-----DDD-----DNNTNE 232
 OY 486 NVINKOEHDIKOKTOIPLOARELITLIVKGAANIFKNCLEIDSTLYKNEFVDKNM 545
 Db 233 NV-----DDDI----- 238
 OY 546 KYIPTEDVSGLSLEBQLRLQEBRTCKVCMDREVSVPFPCGHLVWCOBCAPSL-RKCP1 604
 Db 239 -----EKEYECKVCLERORDAVLMPCRHCVACVQCYGGLQKCP1 278
 OY 605 CPGIKGIVRTFL 617
 Db 279 CRQDVVDPIKIFV 291

RESULT 14

T43523

cut17 protein - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe

C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 02-Jun-2000

C:Accession: T43523; T41649; T41700
 R:Morishita, J.; Matsusaka, T.; Yanagida, M.
 Submitted to the EMBL Data Library, August 1999

A:Description: Fission yeast cut17 is required for chromosome segregation.

A:Reference number: 222536

A:Accession: T43523

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-997 <MOR>

A:Cross-references: EMBL:AB031034; PIDN:BA83415.1

R:Harris, D.; Wood, V.; Rajandream, M.A.; Bartell, B.G.

submitted to the EMBL Data Library, August 1998

A:Reference number: 222007

A:Accession: T41649

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-997 <HAR>

A:Cross-references: EMBL:AL031323; PIDN:CAA20434.1; GSPDB:GNO0068; SPDB:SPCC962.02c

A:Experimental source: strain 972h; cosmid c962

R:Medler, H.; Duesterhoeft, A.; McDougall, R.C.; Rajandream, M.A.; Bartell, B.G.

submitted to the EMBL Data Library, October 1999

A:Reference number: 222010

A:Accession: T41700

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 932-997 <MED>

A:Cross-references: EMBL:AL121899; PIDN:CA858376.1; GSPDB:GNO0068; SPDB:SPCC962.02c

C:Genetics:

A:Gene: cut17; SPCC962.02c; SPDB:SPCC962.02c

A:Map position: 3L

A:Introns: 43/3

Query Match 7.2%; Score 237.5; DB 2; Length 997;
 Best Local Similarity 23.1%; Pred. No. 2.7e-08;
 Matches 106; Conservative 63; Mismatches 196; Indels 93; Gaps 22;

OY 164 RAVEDISSSPFNDYVAMSTEARFLYH--MMPULTFSLPSLARAGFY--IGPG---- 215
 Db 2 KPISSSRKRMNFRREKCNYSKRLDTFOKKWPRAKPPTFLATVAGFYVNPISSESSSE 61
 OY 216 --DRVACFACGKLSNNEPKDAMSEHRHFPNCFLENSLETFLRSISNLSMOTHA-- 271
 Db 62 RLDVNTCYMCKTFYWMEDDDPLKEHTHSPSPW-----AYILSSKNPNQNAL 116
 OY 272 --RMRTFM--VMP-----SSVVPPEOLASAGFY--VGRNDVKCFCDGGRKMEG 319
 Db 117 TKRGEQFVFKVYPRYNNREDYHCEBSVMAASGFVYNPTRDAKDAHLCYODILNHWERD 176
 OY 320 DDPVVEHAKMPRCFELIRMGQFVVEIOGRPHILE---QLLSTSDTTEE-NADPP 374
 Db 177 DDPTEHKKRRADCV-----FTWKDPSLSFTKLSFLSTSNIDPDLTEDNS 224
 OY 375 TIHFGSESSSDAVMM-TPVYKSALE-MGFNRDLYKQTVOSK-----TL 418
 Db 225 ILVSPFPRDSTKSHATLNFSPSRKNLNARLMTSLYTTSEKOSQPTAPAPSPKPKL 284
 OY 419 TTGENYK-----TVNDIVSALLNADEKREKQAEEMASDLSLIRKNRMA 467
 Db 285 LTAPRRKKNPKPKSPKPAVFKPKPFFSDEDDDDDLTAQPSKICNDISQVAKNN-- 341
 OY 468 LFOOLLTCVPLDNLKAVINKOEHDIKOKTOIPLOARELITLIVKGAANIFKNC 527
 Db 342 -----FTETETPKED-----EKDNELEH--LVSPATSVHTVSDITGHQSVTDSDEQ--NNC 390
 OY 528 LK-----EIDSTLYKNEFVDKNMKYIPEVSGISLE 560
 Db 391 MSTPKIEISKEIEFISVSKSKET--SSVSSVGRQ 427

RESULT 15

D36828

orf13 protein - Autographa californica nuclear polyhedrosis virus

C:Species: Autographa californica nuclear polyhedrosis virus, ACNMPV
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 17-Nov-2000
C:Accession: D36828; C72853
R:Brünnagel, S.C.; Daniel, K.D.; Rellly, L.M.; Guarino, L.A.; Hong, T.; Summers, M.D.
Virology 191, 1003-1008, 1992
A:Title: Sequence, genomic organization of the EcoRI-A fragment of Autographa californica
VP8 of reovirus
A:Reference number: A44221; MUID:93079853
A:Accession: D36828
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-286

A:Cross-references: GB:S52569
R:Byers, M.D.; Howard, S.C.; Kuzio, J.; Lopez-Ferber, M.; Possee, R.D.
Virology 202, 586-605, 1994
A:Title: The complete DNA sequence of Autographa californica nuclear polyhedrosis virus.
A:Reference number: A72850; MUID:94303173
A:Accession: C72853
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-199, 'L', 201-286 <AVR>
A:Cross-references: GB:I22858; MUID:9510708; PIDN:AAA6657.1; PID:9559096
C:Genetics:
A:Gene: AC-IAP1
C:Superfamily: viral apoptosis inhibitor IAP; RING finger homology

Query Match 7.28; Score 235.5; DB 2; Length 286;
Best Local Similarly 17.68; Pred. No. 5.9e-09;
Matches 83; Conservative 47; Mismatches 112; Indels 229; Gaps 11;
OY 173 RTNPYSYAMSTEARFLTYHMWPL--TFSPSELRARAFYICGPDRAVACAGKLSN 229
DB 18 RDNRTAHVYDMLIERHSSPENYPIENTAFI--NSLIYNGFKYNGVDHVCYCEAEIKN 75
OY 230 WEPKXDAWSEHRRHPCPLNSLETLEFS-----ISNLSMOT 268
DB 76 MSDEDCIEYAVTSLPYCNANKIARESFQDNITINAVLYKESKRCYKCMNLQ--- 132
OY 269 HAARMRTFM-TYPSVYPVQPEQLASNGFYVGRNDYKCFCCDGLRCHESGDDRWYENH 327
DB 133 --SNMDTFVNFPAALMDITNIAEAGLTFTGRGDETVCFCDCCVQDMHTWEDWQRHA 190
OY 328 KWFPRCEFLIRKKGOEYVDEIQGRPHLLDQLSTDPGTGEENADPPIIHFGPCSSSED 387
DB 191 AENPQCYFVXSVKGRFC----- 208
OY 388 AVNMNTPVVKSALEMGFNRDLVKQTVQSKILTSEMYKTVNDIVSALLMADEKREEKE 447
DB 209 -----ONSITVTNV-----DKRDD-- 222
OY 448 KQAEKASDLSLIRKNMALFOOLTVCVLPIDMLKANYINKOEHDIIKOKTOIPLQAR 507
DB 223 -----DNL-----NENADDI----- 232
OY 508 ELIDTLVKGNAANIFKNCLKEIDSTLVKNLFDKNNKXIPTEVSGISLEQLRRLOE 567
DB 233 -----EE 234
OY 568 ERTCKVMDKEVSVFIPCGHLVVGQECAPSL-RKCPICGRIKGTVRFTL 617
DB 235 KYECKVCLERQDAVLMPCRHFCVQCFGLDQKCPCTCRQDVTDPKIKIFV 285

Search completed: January 7, 2002, 15:49:07
Job time: 701 sec